

## SEQUENCE LISTING

&lt;110&gt; Ruey S. Liou

&lt;120&gt; ANTI-IGE GENE THERAPY

<130> 99-5

<150> 60/100,639

<151> 1998-09-16

<160> 27

<170> FastSEQ for Windows Version 4.0

<210> 1

**<211> 21**

<212> DNA

<213> primer

<400> 1

tcccaggtgc agctgggtgca g

21

<210> 2

<211> 19

<212> DNA

<213> primer

<400> 2

ctgagctcac ggtcaccag

19

**<210> 3**

<211> 21

<212> DNA

<213> primer

<400> 3

tccgacatcc tgctgacca g

21

<211> 19

<212> DNA

<213> primer

**<400> 4**

gtttgatctc caccttqgt

19

**<210> 5**

**<211> 85**

**<212> DNA**

<213> primer

**<400> 5**

ccctggtgac cgtgagctca ggtggcggtg gctcgggcgg tggtaggtcg ggtggcggcg

60

gatctgacat cctgctgacc cagag

85

**SECRET**

<210> 6  
<211> 15  
<212> DNA  
<213> primer

<400> 6  
ggggs ggggs ggggs

15

<210> 7  
<211> 35  
<212> DNA  
<213> primer

<400> 7  
gcggcccagc cggcccaggt gcagctggtg cagag

35

<210> 8  
<211> 34  
<212> DNA  
<213> primer

<400> 8  
ctgcggccgc ttgatctcc accttggtgc cctg

34

<210> 9  
<211> 38  
<212> DNA  
<213> primer

<400> 9  
tcccaagctt tcaccatgca ggtgcagctg gtgcagag

38

<210> 10  
<211> 33  
<212> DNA  
<213> primer

<400> 10  
cccgtcgcg tcatttgatc tccaccttgg tgc

33

<211> 34  
<212> DNA  
<213> primer

<400> 11  
tcccagatct aagcttgccg ccaccatgga ctgg

34

<210> 12  
<211> 22  
<212> DNA  
<213> primer

<400> 12  
gctgatctcg cccacccact cc

22

09091470-112001

<210> 13  
<211> 30  
<212> DNA  
<213> primer

<400> 13  
cccgagatct cgagtcattt gatctccacc

30

<210> 14  
<211> 27  
<212> DNA  
<213> primer

<400> 14  
ggagatctcc acagtccttg aacacac

27

<210> 15  
<211> 21  
<212> DNA  
<213> primer

<400> 15  
tcatttacct ggagacaggg a

21

<210> 16  
<211> 21  
<212> DNA  
<213> primer

<400> 16  
ctaactctt cccctgttga a

21

<210> 17  
<211> 27  
<212> DNA  
<213> primer

<400> 17  
tgaagaaagc ttgccgccac catggag

27

<210> 18

<212> DNA  
<213> primer

<400> 18  
gcacccgctc gtttgatctc caccttgg

29

<210> 19  
<211> 38  
<212> DNA  
<213> primer

<400> 19  
cggaattcga gcggatgctg caccaactgt atcgatct

38

<210> 20

090911 041650

tgg ggc cag ggc acc ctg gtg acc gtg agc tca 369  
 Trp Gly Gln Gly Thr Leu Val Thr Val Ser  
 115 120

**SECRET**

[illegible]

Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ala
1				5					10					15	
Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Ser	Met	Tyr
			20					25					30		
Trp	Leu	Glu	Trp	Val	Arg	Gln	Ala	Pro	Gly	His	Gly	Leu	Glu	Trp	Val
		35					40					45			
Gly	Glu	Ile	Ser	Pro	Gly	Thr	Phe	Thr	Thr	Asn	Tyr	Asn	Glu	Lys	Phe
	50					55				60					
Lys	Ala	Arg	Ala	Thr	Phe	Thr	Ala	Asp	Thr	Ser	Thr	Asn	Thr	Ala	Tyr
65					70					75				80	
Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
			85						90					95	
Ala	Arg	Phe	Ser	His	Phe	Ser	Gly	Ser	Asn	Tyr	Asp	Tyr	Phe	Asp	Tyr
			100					105					110		
Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser						
		115					120								

```
<220>
<221> CDS
<222> (1) ... (321)
```

gac Asp 1	atc Ile	ctg Leu	ctg Leu	acc Thr 5	cag Gln	agc Ser	ccc Pro	ggc Gly	acc Thr 10	ctg Leu	agc Ser	ctg Leu	agc Ser	ccc Pro 15	ggc Gly	48
gag Glu	agg Arg	gcc Ala	acc Thr 20	ctg Leu	agc Ser	tgc Cys	agg Arg	gcc Ala 25	agc Ser	cag Gln	agc Ser	atc Ile	ggc Gly 30	acc Thr	aac Asn	96
atc Ile	cac His	tgg Trp 35	tac Tyr	cag Gln	cag Gln	aag Lys	ccc Pro 40	ggc Gly	cag Gln	gcc Ala	ccc Pro	agg Arg 45	ctg Leu	ctg Leu	atc Ile	144
aag Lys	tac Tyr 50	gcc Ala	agc Ser	gag Glu	agc Ser	atc Ile 55	agc Ser	ggc Gly	atc Ile	ccc Pro	agc Ser 60	agg Arg	ttc Phe	agc Ser	ggc Gly	192
agc Ser 65	ggc Gly	agc Ser	ggc Gly	acc Thr 70	gac Asp	ttc Phe	acc Thr	ctg Leu	acc Thr 75	atc Ile	agc Ser	agg Arg	ctg Leu	gag Glu 80	ccc Pro	240
gag Glu	gac Asp	ttc Phe	gcc Ala 85	atg Met	tac Tyr	tac Tyr	tgc Cys	cag Gln 90	cag Gln	agc Ser	gac Asp	agc Ser	tgg Trp 95	ccc Pro	acc Thr	288

321

<400>	25															
Asp	Ile	Leu	Leu	Thr	Gln	Ser	Pro	Gly	Thr	Leu	Ser	Leu	Ser	Pro	Gly	
1				5					10					15		
Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser	Ile	Gly	Thr	Asn	
			20					25					30			
Ile	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu	Ile	
		35					40					45				
Lys	Tyr	Ala	Ser	Glu	Ser	Ile	Ser	Gly	Ile	Pro	Ser	Arg	Phe	Ser	Gly	
	50					55					60					
Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Arg	Leu	Glu	Pro	
65					70					75				80		
Glu	Asp	Phe	Ala	Met	Tyr	Tyr	Cys	Gln	Gln	Ser	Asp	Ser	Trp	Pro	Thr	
				85					90					95		
Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys						
			100					105								

```
<220>  
<221> CDS  
<222> (1) ... (735)
```

48

144

192

240

atg gag ctg agc agc ctg agg agc gag gac acc gcc gtg tac tac tgc 288  
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

gcc agg ttc agc cac ttc agc ggc agc aac tac gac tac ttc gac tac 336  
Ala Arg Phe Ser His Phe Ser Gly Ser Asn Tyr Asp Tyr Phe Asp Tyr  
100 105 110

tgg ggc cag ggc acc ctg gtg acc gtg agc tca ggt ggc ggt ggc tgc 384  
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser  
115 120 125

ggc ggt ggt ggg tgc ggt ggc ggc gga tct gac atc ctg ctg acc cag 432  
Gly Gly Gly Gly Ser Gly Gly Gly Ser Asp Ile Leu Leu Thr Gln  
130 135 140

agc ccc ggc acc ctg agc ctg agc ccc ggc gag agg gcc acc ctg agc 480  
Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser  
145 150 155 160

tgc agg gcc agc cag agc atc ggc acc aac atc cac tgg tac cag cag 528  
Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn Ile His Trp Tyr Gln Gln  
165 170 175

aag ccc ggc cag gcc ccc agg ctg ctg atc aag tac gcc agc gag agc 576  
Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Lys Tyr Ala Ser Glu Ser  
180 185 190

atc agc ggc atc ccc agc agg ttc agc ggc agc ggc agc ggc acc gac 624  
Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp  
195 200 205

ttc acc ctg acc atc agc agg ctg gag ccc gag gac ttc gcc atg tac 672  
Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Met Tyr  
210 215 220

tac tgc cag cag agc gac agc tgg ccc acc acc ttc ggc cag ggc acc 720  
Tyr Cys Gln Gln Ser Asp Ser Trp Pro Thr Thr Phe Gly Gln Gly Thr  
225 230 235 240

Lys Val Glu Ile Lys 735  
245

<210> 27

<211> 245

<212> PRT

<213> human/murine

<400> 27

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala  
1 5 10 15  
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Met Tyr  
20 25 30  
Trp Leu Glu Trp Val Arg Gln Ala Pro Gly His Gly Leu Glu Trp Val  
35 40 45

0990147013001

Gly	Glu	Ile	Ser	Pro	Gly	Thr	Phe	Thr	Thr	Asn	Tyr	Asn	Glu	Lys	Phe
50						55					60				
Lys	Ala	Arg	Ala	Thr	Phe	Thr	Ala	Asp	Thr	Ser	Thr	Asn	Thr	Ala	Tyr
65					70					75					80
Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
			85						90					95	
Ala	Arg	Phe	Ser	His	Phe	Ser	Gly	Ser	Asn	Tyr	Asp	Tyr	Phe	Asp	Tyr
			100						105					110	
Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser
		115					120						125		
Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Asp	Ile	Leu	Leu	Thr	Gln
		130				135					140				
Ser	Pro	Gly	Thr	Leu	Ser	Leu	Ser	Pro	Gly	Glu	Arg	Ala	Thr	Leu	Ser
145					150					155					160
Cys	Arg	Ala	Ser	Gln	Ser	Ile	Gly	Thr	Asn	Ile	His	Trp	Tyr	Gln	Gln
				165					170					175	
Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu	Ile	Lys	Tyr	Ala	Ser	Glu	Ser
			180						185					190	
Ile	Ser	Gly	Ile	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp
		195					200						205		
Phe	Thr	Leu	Thr	Ile	Ser	Arg	Leu	Glu	Pro	Glu	Asp	Phe	Ala	Met	Tyr
		210				215					220				
Tyr	Cys	Gln	Gln	Ser	Asp	Ser	Trp	Pro	Thr	Thr	Phe	Gly	Gln	Gly	Thr
225					230					235					240
Lys	Val	Glu	Ile	Lys											
				245											

09991470-112001